

SEQUENCE LISTING

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Hideki ENDOH

<120> METHOD FOR SCREENING AN AGENT FOR IMPROVING INSULIN RESISTANCE

<130> Q85576

<150> PCT/JP03/08367

<151> 2003-07-01

<150> JP 2002-193814

<151> 2002-07-02

<160> 16

<170> PatentIn version 3.1

<210> 1

<211> 1845

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1) .. (1845)

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ggg	gca	cct	cga	ttt	gga	gga	agt	agg	gca	ggg	ccc	tta	tct	gga	aag	96
Gly	Ala	Pro	Arg	Phe	Gly	Gly	Ser	Arg	Ala	Gly	Pro	Leu	Ser	Gly	Lys	
			20					25					30			

aag	ttt	gga	aac	cct	ggg	gag	aaa	tta	gtt	aaa	aag	aag	tgg	aat	ctt	144
Lys	Phe	Gly	Asn	Pro	Gly	Glu	Lys	Leu	Val	Lys	Lys	Lys	Trp	Asn	Leu	
		35					40					45				

gat	gag	ctg	cct	aaa	ttt	gag	aag	aat	ttt	tat	caa	gag	cac	cct	gat	192
Asp	Glu	Leu	Pro	Lys	Phe	Glu	Lys	Asn	Phe	Tyr	Gln	Glu	His	Pro	Asp	
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ttg	gct	agg	cgc	aca	gca	caa	gag	gtg	gaa	aca	tac	aga	aga	agc	aag	240
Leu	Ala	Arg	Arg	Thr	Ala	Gln	Glu	Val	Glu	Thr	Tyr	Arg	Arg	Ser	Lys	
65				70					75					80		

gaa	att	aca	gtt	aga	ggg	cac	aac	tgc	ccg	aag	cca	gtt	cta	aat	ttt	288
Glu	Ile	Thr	Val	Arg	Gly	His	Asn	Cys	Pro	Lys	Pro	Val	Leu	Asn	Phe	
			85					90					95			

tat	gaa	gcc	aat	ttc	cct	gca	aat	gtc	atg	gat	gtt	att	gca	aga	cag	336
Tyr	Glu	Ala	Asn	Phe	Pro	Ala	Asn	Val	Met	Asp	Val	Ile	Ala	Arg	Gln	
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aat ttc act gaa ccc act gct att caa gct cag gga tgg cca gtt gct Asn Phe Thr Glu Pro Thr Ala Ile Gln Ala Gln Gly Trp Pro Val Ala 115 120 125	384
cta agt gga ttg gat atg gtt gga gtg gca cag act gga tct ggg aaa Leu Ser Gly Leu Asp Met Val Gly Val Ala Gln Thr Gly Ser Gly Lys 130 135 140	432
aca ttg tct tat ttg ctt cct gcc att gtc cac atc aat cat cag cca Thr Leu Ser Tyr Leu Leu Pro Ala Ile Val His Ile Asn His Gln Pro 145 150 155 160	480
ttc cta gag aga ggc gat ggg cct att tgt ttg gtg ctg gca cca act Phe Leu Glu Arg Gly Asp Gly Pro Ile Cys Leu Val Leu Ala Pro Thr 165 170 175	528
cgg gaa ctg gcc caa cag gtg cag caa gta gct gct gaa tat tgt aga Arg Glu Leu Ala Gln Gln Val Gln Gln Val Ala Ala Glu Tyr Cys Arg 180 185 190	576
gca tgt cgc ttg aag tct act tgt atc tac ggt ggt gct cct aag gga Ala Cys Arg Leu Lys Ser Thr Cys Ile Tyr Gly Gly Ala Pro Lys Gly 195 200 205	624
cca caa ata cgt gat ttg gag aga ggt gtg gaa atc tgt att gca aca Pro Gln Ile Arg Asp Leu Glu Arg Gly Val Glu Ile Cys Ile Ala Thr 210 215 220	672
cct gga aga ctg att gac ttt tta gag tgt gga aaa acc aat ctg aga Pro Gly Arg Leu Ile Asp Phe Leu Glu Cys Gly Lys Thr Asn Leu Arg 225 230 235 240	720
aga aca acc tac ctt gtc ctt gat gaa gca gat aga atg ctt gat atg Arg Thr Thr Tyr Leu Val Leu Asp Glu Ala Asp Arg Met Leu Asp Met 245 250 255	768
ggc ttt gaa ccc caa ata agg aag att gtg gat caa ata aga cct gat Gly Phe Glu Pro Gln Ile Arg Lys Ile Val Asp Gln Ile Arg Pro Asp 260 265 270	816
agg caa act cta atg tgg agt gcg act tgg cca aaa gaa gta aga cag Arg Gln Thr Leu Met Trp Ser Ala Thr Trp Pro Lys Glu Val Arg Gln 275 280 285	864
ctt gct gaa gat ttc ctg aaa gac tat att cat ata aac att ggt gca Leu Ala Glu Asp Phe Leu Lys Asp Tyr Ile His Ile Asn Ile Gly Ala 290 295 300	912
ctt gaa ctg agt gca aac cac aac att ctt cag att gtg gat gtg tgt Leu Glu Leu Ser Ala Asn His Asn Ile Leu Gln Ile Val Asp Val Cys 305 310 315 320	960
cat gac gta gaa aag gat gaa aaa ctt att cgt cta atg gaa gag atc His Asp Val Glu Lys Asp Glu Lys Leu Ile Arg Leu Met Glu Glu Ile 325 330 335	1008
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atg	ggg	atc	cat	ggg	gac	aag	agt	caa	caa	gag	cgt	gac	tgg	gtt	cta	1152
Met	Gly	Ile	His	Gly	Asp	Lys	Ser	Gln	Gln	Glu	Arg	Asp	Trp	Val	Leu	
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aat	gaa	ttc	aaa	cat	gga	aaa	gct	cct	att	ctg	att	gct	aca	gat	gtg	1200
Asn	Glu	Phe	Lys	His	Gly	Lys	Ala	Pro	Ile	Leu	Ile	Ala	Thr	Asp	Val	
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gcc	tcc	aga	ggg	cta	gat	gtg	gaa	gat	gtg	aaa	ttt	gtc	atc	aat	tat	1248
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gac	tac	cct	aac	tcc	tca	gag	gat	tat	att	cat	cga	att	gga	aga	act	1296
Asp	Tyr	Pro	Asn	Ser	Ser	Glu	Asp	Tyr	Ile	His	Arg	Ile	Gly	Arg	Thr	
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Ala	Arg	Ser	Thr	Lys	Thr	Gly	Thr	Ala	Tyr	Thr	Phe	Phe	Thr	Pro	Asn	
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Asn	Ile	Lys	Gln	Val	Ser	Asp	Leu	Ile	Ser	Val	Leu	Arg	Glu	Ala	Asn	
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Gln	Ala	Ile	Asn	Pro	Lys	Leu	Leu	Gln	Leu	Val	Glu	Asp	Arg	Gly	Ser	
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ggg	cgt	tcc	agg	ggg	aga	gga	ggc	atg	aag	gat	gac	cgt	cgg	gac	aga	1488
Gly	Arg	Ser	Arg	Gly	Arg	Gly	Gly	Met	Lys	Asp	Asp	Arg	Arg	Asp	Arg	
				485				490						495		
tac	tct	gcg	ggc	aaa	agg	ggg	gga	ttt	aat	acc	ttt	aga	gac	agg	gaa	1536
Tyr	Ser	Ala	Gly	Lys	Arg	Gly	Gly	Phe	Asn	Thr	Phe	Arg	Asp	Arg	Glu	
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aat	tat	gac	aga	ggg	tac	tct	agc	ctg	ctt	aaa	aga	gat	ttt	ggg	gca	1584
Asn	Tyr	Asp	Arg	Gly	Tyr	Ser	Ser	Leu	Leu	Lys	Arg	Asp	Phe	Gly	Ala	
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aaa	act	cag	aat	ggg	gtt	tac	agt	gct	gca	aat	tac	acc	aat	ggg	agc	1632
Lys	Thr	Gln	Asn	Gly	Val	Tyr	Ser	Ala	Ala	Asn	Tyr	Thr	Asn	Gly	Ser	
	530					535					540					
ttt	gga	agt	aat	ttt	gtg	tct	gct	ggg	ata	cag	acc	agt	ttt	agg	act	1680
Phe	Gly	Ser	Asn	Phe	Val	Ser	Ala	Gly	Ile	Gln	Thr	Ser	Phe	Arg	Thr	
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Gly	Asn	Pro	Thr	Gly	Thr	Tyr	Gln	Asn	Gly	Tyr	Asp	Ser	Thr	Gln	Gln	
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tac	gga	agt	aat	gtt	cca	aat	atg	cac	aat	ggg	atg	aac	caa	cag	gca	1776
Tyr	Gly	Ser	Asn	Val	Pro	Asn	Met	His	Asn	Gly	Met	Asn	Gln	Gln	Ala	
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tat gca tat cct gct act gca gct gca cct atg att ggt tat cca atg	1824
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595 600 605	

cca aca gga tat tcc caa taa	1845
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Lys Phe Gly Asn Pro Gly Glu Lys Leu Val Lys Lys Lys Trp Asn Leu
35 40 45

Asp Glu Leu Pro Lys Phe Glu Lys Asn Phe Tyr Gln Glu His Pro Asp
50 55 60

Leu Ala Arg Arg Thr Ala Gln Glu Val Glu Thr Tyr Arg Arg Ser Lys
65 70 75 80

Glu Ile Thr Val Arg Gly His Asn Cys Pro Lys Pro Val Leu Asn Phe
85 90 95

Tyr Glu Ala Asn Phe Pro Ala Asn Val Met Asp Val Ile Ala Arg Gln
100 105 110

Asn Phe Thr Glu Pro Thr Ala Ile Gln Ala Gln Gly Trp Pro Val Ala
115 120 125

Leu Ser Gly Leu Asp Met Val Gly Val Ala Gln Thr Gly Ser Gly Lys
130 135 140

Thr Leu Ser Tyr Leu Leu Pro Ala Ile Val His Ile Asn His Gln Pro
145 150 155 160

Phe Leu Glu Arg Gly Asp Gly Pro Ile Cys Leu Val Leu Ala Pro Thr
165 170 175

Arg Glu Leu Ala Gln Gln Val Gln Gln Val Ala Ala Glu Tyr Cys Arg
 180 185 190

Ala Cys Arg Leu Lys Ser Thr Cys Ile Tyr Gly Gly Ala Pro Lys Gly
 195 200 205

Pro Gln Ile Arg Asp Leu Glu Arg Gly Val Glu Ile Cys Ile Ala Thr
 210 215 220

Pro Gly Arg Leu Ile Asp Phe Leu Glu Cys Gly Lys Thr Asn Leu Arg
 225 230 235 240

Arg Thr Thr Tyr Leu Val Leu Asp Glu Ala Asp Arg Met Leu Asp Met
 245 250 255

Gly Phe Glu Pro Gln Ile Arg Lys Ile Val Asp Gln Ile Arg Pro Asp
 260 265 270

Arg Gln Thr Leu Met Trp Ser Ala Thr Trp Pro Lys Glu Val Arg Gln
 275 280 285

Leu Ala Glu Asp Phe Leu Lys Asp Tyr Ile His Ile Asn Ile Gly Ala
 290 295 300

Leu Glu Leu Ser Ala Asn His Asn Ile Leu Gln Ile Val Asp Val Cys
 305 310 315 320

His Asp Val Glu Lys Asp Glu Lys Leu Ile Arg Leu Met Glu Glu Ile
 325 330 335

Met Ser Glu Lys Glu Asn Lys Thr Ile Val Phe Val Glu Thr Lys Arg
 340 345 350

Arg Cys Asp Glu Leu Thr Arg Lys Met Arg Arg Asp Gly Trp Pro Ala
 355 360 365

Met Gly Ile His Gly Asp Lys Ser Gln Gln Glu Arg Asp Trp Val Leu
 370 375 380

Asn Glu Phe Lys His Gly Lys Ala Pro Ile Leu Ile Ala Thr Asp Val
 385 390 395 400

Ala Ser Arg Gly Leu Asp Val Glu Asp Val Lys Phe Val Ile Asn Tyr
 405 410 415

Asp Tyr Pro Asn Ser Ser Glu Asp Tyr Ile His Arg Ile Gly Arg Thr
420 425 430

Ala Arg Ser Thr Lys Thr Gly Thr Ala Tyr Thr Phe Phe Thr Pro Asn
435 440 445

Asn Ile Lys Gln Val Ser Asp Leu Ile Ser Val Leu Arg Glu Ala Asn
450 455 460

Gln Ala Ile Asn Pro Lys Leu Leu Gln Leu Val Glu Asp Arg Gly Ser
465 470 475 480

Gly Arg Ser Arg Gly Arg Gly Gly Met Lys Asp Asp Arg Arg Asp Arg
485 490 495

Tyr Ser Ala Gly Lys Arg Gly Gly Phe Asn Thr Phe Arg Asp Arg Glu
500 505 510

Asn Tyr Asp Arg Gly Tyr Ser Ser Leu Leu Lys Arg Asp Phe Gly Ala
515 520 525

Lys Thr Gln Asn Gly Val Tyr Ser Ala Ala Asn Tyr Thr Asn Gly Ser
530 535 540

Phe Gly Ser Asn Phe Val Ser Ala Gly Ile Gln Thr Ser Phe Arg Thr
545 550 555 560

Gly Asn Pro Thr Gly Thr Tyr Gln Asn Gly Tyr Asp Ser Thr Gln Gln
565 570 575

Tyr Gly Ser Asn Val Pro Asn Met His Asn Gly Met Asn Gln Gln Ala
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Tyr Ala Tyr Pro Ala Thr Ala Ala Ala Pro Met Ile Gly Tyr Pro Met
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Pro Thr Gly Tyr Ser Gln
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ttc act gat aca ctg tct gca aac ata tca caa gaa atg acc atg gtt	96
Phe Thr Asp Thr Leu Ser Ala Asn Ile Ser Gln Glu Met Thr Met Val	
20 25 30	
gac aca gag atg cca ttc tgg ccc acc aac ttt ggg atc agc tcc gtg	144
Asp Thr Glu Met Pro Phe Trp Pro Thr Asn Phe Gly Ile Ser Ser Val	
35 40 45	
gat ctc tcc gta atg gaa gac cac tcc cac tcc ttt gat atc aag ccc	192
Asp Leu Ser Val Met Glu Asp His Ser His Ser Phe Asp Ile Lys Pro	
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ttc act act gtt gac ttc tcc agc att tct act cca cat tac gaa gac	240
Phe Thr Thr Val Asp Phe Ser Ser Ile Ser Thr Pro His Tyr Glu Asp	
65 70 75 80	
att cca ttc aca aga aca gat cca gtg gtt gca gat tac aag tat gac	288
Ile Pro Phe Thr Arg Thr Asp Pro Val Val Ala Asp Tyr Lys Tyr Asp	
85 90 95	
ctg aaa ctt caa gag tac caa agt gca atc aaa gtg gag cct gca tct	336
Leu Lys Leu Gln Glu Tyr Gln Ser Ala Ile Lys Val Glu Pro Ala Ser	
100 105 110	
cca cct tat tat tct gag aag act cag ctc tac aat aag cct cat gaa	384
Pro Pro Tyr Tyr Ser Glu Lys Thr Gln Leu Tyr Asn Lys Pro His Glu	
115 120 125	
gag cct tcc aac tcc ctc atg gca att gaa tgt cgt gtc tgt gga gat	432
Glu Pro Ser Asn Ser Leu Met Ala Ile Glu Cys Arg Val Cys Gly Asp	
130 135 140	
aaa gct tct gga ttt cac tat gga gtt cat gct tgt gaa gga tgc aag	480
Lys Ala Ser Gly Phe His Tyr Gly Val His Ala Cys Glu Gly Cys Lys	
145 150 155 160	
ggg ttc ttc cgg aga aca atc aga ttg aag ctt atc tat gac aga tgt	528
Gly Phe Phe Arg Arg Thr Ile Arg Leu Lys Leu Ile Tyr Asp Arg Cys	
165 170 175	
gat ctt aac tgt cgg atc cac aaa aaa agt aga aat aaa tgt cag tac	576
Asp Leu Asn Cys Arg Ile His Lys Lys Ser Arg Asn Lys Cys Gln Tyr	
180 185 190	
tgt cgg ttt cag aaa tgc ctt gca gtg ggg atg tct cat aat gcc atc	624
Cys Arg Phe Gln Lys Cys Leu Ala Val Gly Met Ser His Asn Ala Ile	
195 200 205	
agg ttt ggg cgg atg cca cag gcc gag aag gag aag ctg ttg gcg gag	672
Arg Phe Gly Arg Met Pro Gln Ala Glu Lys Glu Lys Leu Leu Ala Glu	
210 215 220	
atc tcc agt gat atc gac cag ctg aat cca gag tcc gct gac ctc cgg	720

Ile Ser Ser Asp Ile Asp Gln Leu Asn Pro Glu Ser Ala Asp Leu Arg	
225 230 235 240	
gcc ctg gca aaa cat ttg tat gac tca tac ata aag tcc ttc ccg ctg	768
Ala Leu Ala Lys His Leu Tyr Asp Ser Tyr Ile Lys Ser Phe Pro Leu	
245 250 255	
acc aaa gca aag gcg agg gcg atc ttg aca gga aag aca aca gac aaa	816
Thr Lys Ala Lys Ala Arg Ala Ile Leu Thr Gly Lys Thr Thr Asp Lys	
260 265 270	
tca cca ttc gtt atc tat gac atg aat tcc tta atg atg gga gaa gat	864
Ser Pro Phe Val Ile Tyr Asp Met Asn Ser Leu Met Met Gly Glu Asp	
275 280 285	
aaa atc aag ttc aaa cac atc acc ccc ctg cag gag cag agc aaa gag	912
Lys Ile Lys Phe Lys His Ile Thr Pro Leu Gln Glu Gln Ser Lys Glu	
290 295 300	
gtg gcc atc cgc atc ttt cag ggc tgc cag ttt cgc tcc gtg gag gct	960
Val Ala Ile Arg Ile Phe Gln Gly Cys Gln Phe Arg Ser Val Glu Ala	
305 310 315 320	
gtg cag gag atc aca gag tat gcc aaa agc att cct ggt ttt gta aat	1008
Val Gln Glu Ile Thr Glu Tyr Ala Lys Ser Ile Pro Gly Phe Val Asn	
325 330 335	
ctt gac ttg aac gac caa gta act ctc ctc aaa tat gga gtc cac gag	1056
Leu Asp Leu Asn Asp Gln Val Thr Leu Leu Lys Tyr Gly Val His Glu	
340 345 350	
atc att tac aca atg ctg gcc tcc ttg atg aat aaa gat ggg gtt ctc	1104
Ile Ile Tyr Thr Met Leu Ala Ser Leu Met Asn Lys Asp Gly Val Leu	
355 360 365	
ata tcc gag ggc caa ggc ttc atg aca agg gag ttt cta aag agc ctg	1152
Ile Ser Glu Gly Gln Gly Phe Met Thr Arg Glu Phe Leu Lys Ser Leu	
370 375 380	
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Arg Lys Pro Phe Gly Asp Phe Met Glu Pro Lys Phe Glu Phe Ala Val	
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Lys Phe Asn Ala Leu Glu Leu Asp Asp Ser Asp Leu Ala Ile Phe Ile	
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gct gtc att att ctc agt gga gac cgc cca ggt ttg ctg aat gtg aag	1296
Ala Val Ile Ile Leu Ser Gly Asp Arg Pro Gly Leu Leu Asn Val Lys	
420 425 430	
ccc att gaa gac att caa gac aac ctg cta caa gcc ctg gag ctc cag	1344
Pro Ile Glu Asp Ile Gln Asp Asn Leu Leu Gln Ala Leu Glu Leu Gln	
435 440 445	
ctg aag ctg aac cac cct gag tcc tca cag ctg ttt gcc aag ctg ctc	1392
Leu Lys Leu Asn His Pro Glu Ser Ser Gln Leu Phe Ala Lys Leu Leu	
450 455 460	
cag aaa atg aca gac ctc aga cag att gtc acg gaa cac gtg cag cta	1440

Gln Lys Met Thr Asp Leu Arg Gln Ile Val Thr Glu His Val Gln Leu
 465 470 475 480

 ctg cag gtg atc aag aag acg gag aca gac atg agt ctt cac ccg ctc 1488
 Leu Gln Val Ile Lys Lys Thr Glu Thr Asp Met Ser Leu His Pro Leu
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 ctg cag gag atc tac aag gac ttg tac tag 1518
 Leu Gln Glu Ile Tyr Lys Asp Leu Tyr
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 Asp Thr Glu Met Pro Phe Trp Pro Thr Asn Phe Gly Ile Ser Ser Val
 35 40 45

 Asp Leu Ser Val Met Glu Asp His Ser His Ser Phe Asp Ile Lys Pro
 50 55 60

 Phe Thr Thr Val Asp Phe Ser Ser Ile Ser Thr Pro His Tyr Glu Asp
 65 70 75 80

 Ile Pro Phe Thr Arg Thr Asp Pro Val Val Ala Asp Tyr Lys Tyr Asp
 85 90 95

 Leu Lys Leu Gln Glu Tyr Gln Ser Ala Ile Lys Val Glu Pro Ala Ser
 100 105 110

 Pro Pro Tyr Tyr Ser Glu Lys Thr Gln Leu Tyr Asn Lys Pro His Glu
 115 120 125

 Glu Pro Ser Asn Ser Leu Met Ala Ile Glu Cys Arg Val Cys Gly Asp
 130 135 140

 Lys Ala Ser Gly Phe His Tyr Gly Val His Ala Cys Glu Gly Cys Lys
 145 150 155 160

 Gly Phe Phe Arg Arg Thr Ile Arg Leu Lys Leu Ile Tyr Asp Arg Cys

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Ala Val Ile Ile Leu Ser Gly Asp Arg Pro Gly Leu Leu Asn Val Lys		
420	425	430
Pro Ile Glu Asp Ile Gln Asp Asn Leu Leu Gln Ala Leu Glu Leu Gln		
435	440	445
Leu Lys Leu Asn His Pro Glu Ser Ser Gln Leu Phe Ala Lys Leu Leu		
450	455	460
Gln Lys Met Thr Asp Leu Arg Gln Ile Val Thr Glu His Val Gln Leu		
465	470	475
Leu Gln Val Ile Lys Lys Thr Glu Thr Asp Met Ser Leu His Pro Leu		
485	490	495
Leu Gln Glu Ile Tyr Lys Asp Leu Tyr		
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ccctggaggt ggacggtttc agtccacaca tactgggacc ccaggagagac actcaccagc	360
atccgagcct gccatgtttc agaggcaggt cgccgccgga ctccgacgcg gccgggaagg	420
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gtgaggtcaa gagagtgcag aatgaggcat tccaatggtg ggtgggcccct gacctgagag	1020
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ccggtctcta gtagtgcagc ttcggctggt gtcacgggtg tccttctctc gctgccgcc	1260
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 ggagagatgg gtggcctgcc atgggtatc 29

 <210> 10
 <211> 41
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: an artificially
 synthesized primer sequence

 <400> 10
 cttctagatc ttattgggaa tatcctgttg gcattggata a 41

 <210> 11
 <211> 18
 <212> DNA
 <213> Mus musculus

 <400> 11
 gcacagcagg tgcagcaa 18

 <210> 12
 <211> 24
 <212> DNA
 <213> Mus musculus

 <400> 12
 gcaccacat agatgcaagt agac 24

 <210> 13
 <211> 20
 <212> DNA
 <213> Mus musculus

 <400> 13
 aaagtggaga ttgttgccat 20

 <210> 14
 <211> 19
 <212> DNA
 <213> Mus musculus

 <400> 14
 ttgactgtgc cgttgaatt 19

<210> 15
<211> 26
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: an artificially
synthesized primer sequence

<400> 15
agggtaccct cagggcccat agcgca

26

<210> 16
<211> 26
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: an artificially
synthesized primer sequence

<400> 16
agctcgagtc gctggaaatg gcctcg

26